

IN THE CLAIMS

Please amend the claims as follows:

Claims 1-45 (Canceled).

Claim 46 (New): A method for high throughput analysis of data sets generally described by sets of peaks characterized by a position and an area.

Claim 47 (New): A method according to claim 46, wherein bioinformatic tools are used to extract and smooth peak data sets according to parameter files and store them in data files.

Claim 48 (New): A method according to claim 46, wherein particular profiles representing peaks are created to be analyzed.

Claim 49 (New): A method according to claim 46, wherein a peak database is built.

Claim 50 (New): A method according to claim 49, wherein the peak database is analyzed by statistical tools.

Claim 51 (New): A method according to claim 50, wherein analysis of the peak database is used to determine prognostic or diagnostic criteria.

Claim 52 (New): A method according to claim 51, wherein the prognostic and diagnostic criteria are used in the field of physiopathology such as immunotherapy, cancer treatment, HIV, infectious disease, autoimmune disease.

Claim 53 (New): A method according to claim 46, wherein the method is a high throughput method for analysis of immune repertoires.

Claim 54 (New): A method according to claim 53, comprising:
starting with biological samples, which contains DNA or RNA fragments,
purifying the DNA or RNA fragments.

Claim 55 (New): The method according to claim 54, further comprising
synthesizing cDNA from purified RNA,
on purified DNA or cDNA, performing amplification of DNA by PCR or SDA
methods by using oligonucleotides specific for antigen specific receptor genes such as
Immunoglobulin and T-cell receptor, variable (V), Junctional (J), and Constant (c) regions,
on amplified DNA, performing a labeling for detection by performing a runoff
extension step with J or C specific oligonucleotide labeled with a fluorescent drug,
on each labeled amplified DNA, an electrophoretic separation is made on an
automatic sequencer,
for each eletrophoregram, identifying peaks by determining their position and area
that correspond to labeled amplified DNA.

Claim 56 (New): A method according to claim 55, wherein the method of analysis is
based on reading of the labeled amplified DNA.

Claim 57 (New): A computer program product, comprising:
a computer storage medium; and

a computer program code mechanism embedded in the computer storage medium for causing a computer to produce an analysis of raw data produced by a separation technique for biomolecules, the computer program code mechanism comprising:

a first computer code device configured to extract a first set of raw data and a second set of raw data from at least one database,

a second computer code device configured to determine a first value from the first set of raw data corresponding to a first characteristic and a second value from the second set of raw data corresponding to the first characteristic, and

a third computer code device configured to store the first value and the second value in a memory.

Claim 58 (New): The computer program product of Claim 57, the computer program code mechanism further comprising:

a fourth computer code device configured to retrieve the first value and the second value from the memory and to order the first value and the second value based on a user preference stored in a second memory.

Claim 59 (New): The computer program product of Claim 58, the computer program code mechanism further comprising:

a fifth computer code device configured to produce a graphical representation of the first value and the second value as ordered by the fourth computer code device,

Claim 60 (New): The computer program product of Claim 58, the computer program code mechanism further comprising:

a fifth computer code device configured to smooth at least one of the first set of raw data and the second set of raw data produced by the separation technique for biomolecules.

Claim 61 (New): The computer program product of Claim 58, the computer program code mechanism further comprising:

a fifth computer code device configured to format at least one of the first value and the second value.

Claim 62 (New): The computer program product of Claim 57, the computer program code mechanism further comprising:

a fourth computer code device configured to parameterize at least one of the first set of raw data and the second set of raw data.

Claim 63 (New): The computer program product of Claim 57, the computer program code mechanism further comprising:

a fourth computer code device configured to analyze at least one of the first set of raw data and the second set of raw data.

Claim 64 (New): The computer program product of Claim 57, the computer program code mechanism further comprising:

a fourth computer code device configured to export at least one of the first value and the second value.

Claim 65 (New): The computer program product of Claim 57, wherein the first characteristic comprises a peak.

Claim 66 (New): The computer program product of Claim 57, wherein the separation technique for biomolecules comprises polynucleotide sequencing.

Claim 67 (New): The computer program product of Claim 66, wherein the polynucleotide is DNA.

Claim 68 (New): A device, comprising:
at least one extractor configured to extract raw data produced by a separation technique for biomolecules, the extractor including:
a processor, and
a computer readable medium encoded with processor readable instructions that, when executed by the processor implement:

an extraction mechanism configured to extract a first set of raw data and a second set of raw data from at least one database,

a characteristic determining mechanism configured to determine a first value from the first set of raw data corresponding to a first characteristic and a second value from the second set of raw data corresponding to the first characteristic, and

an output mechanism configured to store the first value and the second value in a memory.

Claim 69 (New): A system, comprising:
a digital repository populated with entries of raw data produced by a separation technique for biomolecules;

a processor; and

a computer readable medium encoded with processor readable instructions that, when executed by the processor implement:

an extraction mechanism configured to extract a first set of raw data and a second set of raw data from the digital repository,

a characteristic determining mechanism configured to determine a first value from the first set of raw data corresponding to a first characteristic and a second value from the second set of raw data corresponding to the first characteristic, and

an output mechanism configured to store the first value and the second value in a memory.

Claim 70 (New): A system, comprising:

a digital repository populated with entries of raw data produced by a separation technique for biomolecules;

a processor; and

a computer readable medium encoded with processor readable instructions that, when executed by the processor implement:

an extraction mechanism configured to extract a first set of raw data and a second set of raw data from the digital repository via a network,

a characteristic determining mechanism configured to determine a first value from the first set of raw data corresponding to a first characteristic and a second value from the second set of raw data corresponding to the first characteristic, and

an output mechanism configured to store the first value and the second value in a memory.

Claim 71 (New): The system of Claim 70, wherein at least a portion of the network comprises an Internet protocol network.

Claim 72 (New): The system of Claim 71, wherein at least a portion of the network comprises the Internet.

Claim 73 (New): A computer data signal embodied in a carrier wave, said computer data signal comprising extracted raw data produced by a separation technique for biomolecules.

Claim 74 (New): A computer data signal embodied in a carrier wave, said computer data signal comprising:

smoothed raw data, wherein the smoothed raw data includes data produced by a separation technique for biomolecules.

Claim 75 (New): A computer data signal embodied in a carrier wave, said computer data signal comprising:

formatted raw data, wherein the formatted raw data includes data produced by a separation technique for biomolecules.

Claim 76 (New): A computer data signal embodied in a carrier wave, said computer data signal comprising:

parameterized raw data, wherein the parameterized raw data includes data produced by a separation technique for biomolecules.

Claim 77 (New): A computer data signal embodied in a carrier wave, said computer data signal comprising:

analyzed raw data, wherein the analyzed raw data includes data produced by a separation technique for biomolecules.

Claim 78 (New): A computer data signal embodied in a carrier wave, said computer data signal comprising:

exported raw data, wherein the exported raw data includes data produced by a separation technique for biomolecules.

Claim 79 (New): A software package, wherein said software package is embodied by ISEApeaks package 2.0.1.

Claim 80 (New): A method comprising:

- a) isolating a biological sample;
- b) extracting raw data from the biological sample; and
- c) compiling the raw data into a database using ISEApeaks.

Claim 81 (New): The method of Claim 80, wherein said biological sample is selected from the group consisting of a growth culture, an electrophoretic sample, a chromatographic column, a blotting membrane, a centrifugation tube, or a microarray chip.

Claim 82 (New): The method of Claim 80, wherein said biological sample comprises one or more biomolecule.

Claim 83 (New): The method of Claim 82, wherein said biomolecule is selected from the group consisting of intact cells, cellular material, DNA, RNA, and proteins.

Claim 84 (New): The method of Claim 82, wherein said biomolecule is labeled.

Claim 85 (New): The method of Claim 80, wherein said isolating is a technique selected from the group consisting of centrifugation, precipitation, batch adsorption, chromatography, electrophoresis, and a microarray chip.

Claim 86 (New): The method of Claim 80, wherein said extracting comprises using a bioinformatics tool.

Claim 87 (New): The method of Claim 86, wherein said bioinformatics tool is selected from the group consisting of GENESCAN™, MMUNOSCOPE™, GENOTESTER™, IMAGEQUANT™, EAGLESIGHT™, QUANTITYONE™, and MICROARRAY SUITE™.

Claim 88 (New): The method of Claim 80, further comprising analyzing said raw data using ISEApeaks.

Claim 89 (New): A device for diagnostic or prognostic applications comprising:
(a) a set of oligonucleotides for describing TC Receptor or Immunoglobulin repertoires;

(b) a reference database of TC Receptor or Immunoglobulin repertoires data; and

(c) written or informatic guidelines for obtaining results from the sample to be analyzed.

Claim 90 (New): The method according to Claim 80, wherein the biological sample is isolated from a mammal.